SEQUENCE LISTING

(1) GENERAL INFORMATION:

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                Fitchen, John H.

    (ii) TITLE OF INVENTION: NOVEL EPITHELIAL TISSUE IMAGING AGENT

   (iii) NUMBER OF SEQUENCES: 93

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    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE: 9-JAN-1998
        (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:
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        (C) REFERENCE/DOCKET NUMBER: 310098.402

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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 137 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala
1               5                   10                  15

Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp
            20                  25                  30

Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu
            35                  40                  45

Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Pro Val Tyr His
            50                  55                  60

Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp
65                  70                  75                  80

Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser
                85                  90                  95

Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala
                100                 105                 110

Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala
            115                 120                 125

Leu Thr Pro Asp Ala Cys Tyr Pro Asp
        130                 135
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 135 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Gln Asp Glu Asn Glu Arg Ile Val Val Asp Asn Lys Cys Lys Cys Ala
1               5                   10                  15

Arg Ile Thr Ser Arg Ile Ile Pro Ser Ala Glu Asp Pro Ser Gln Asp
            20                  25                  30

Ile Val Glu Arg Asn Val Arg Ile Ile Val Pro Leu Asn Ser Arg Glu
            35                  40                  45

Asn Ile Ser Asp Pro Thr Ser Pro Met Arg Thr Lys Pro Val Tyr His
            50                  55                  60
```

Leu Ser Asp Leu Cys Lys Lys Cys Asp Thr Thr Glu Val Glu Leu Glu
65   70   75   80

Asp Gln Val Val Thr Ala Ser Gln Ser Asn Ile Cys Asp Ser Asp Ala
            85   90   95

Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Asn Arg Val
        100   105   110

Lys Leu Ser Tyr Arg Gly Gln Thr Lys Met Val Glu Thr Ala Leu Thr
        115   120   125

Pro Asp Ser Cys Tyr Pro Asp
    130   135

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 137 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Asp Glu Ala Thr Ile Leu Ala Asp Asn Lys Cys Met Cys Thr Arg
1   5   10   15

Val Thr Ser Arg Ile Ile Pro Ser Thr Glu Asp Pro Asn Glu Asp Ile
            20   25   30

Val Glu Arg Asn Ile Arg Ile Val Val Pro Leu Asn Asn Arg Glu Asn
            35   40   45

Ile Ser Asp Pro Thr Ser Pro Leu Arg Arg Asn Pro Val Tyr His Leu
    50   55   60

Ser Asp Val Cys Lys Lys Cys Asp Pro Val Glu Val Glu Leu Glu Asp
65   70   75   80

Gln Val Val Thr Ala Thr Gln Ser Asn Ile Cys Asn Glu Asp Asp Gly
            85   90   95

Val Pro Glu Thr Cys Tyr Met Tyr Asp Arg Asn Lys Cys Tyr Thr Thr
            100   105   110

Met Val Pro Leu Arg Tyr His Gly Glu Thr Lys Met Val Gln Ala Ala
        115   120   125

```
        Leu Thr Pro Asp Ser Cys Tyr Pro Asp
            130                 135
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 136 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Glu Asp Glu Ser Thr Val Leu Val Asp Asn Lys Cys Gln Cys Val Arg
1               5               10              15

Ile Thr Ser Arg Ile Ile Arg Asp Pro Asp Asn Pro Ser Glu Asp Ile
            20              25              30

Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Thr Arg Glu Asn
            35              40              45

Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Glu Pro Lys Tyr Asn Leu
    50              55              60

Ala Asn Leu Cys Lys Lys Cys Asp Pro Thr Glu Ile Glu Leu Asp Asn
65              70              75              80

Gln Val Phe Thr Ala Ser Gln Ser Asn Ile Cys Pro Asp Asp Asp Tyr
            85              90              95

Ser Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Thr Leu
            100             105             110

Val Pro Ile Thr His Arg Gly Val Thr Arg Met Val Lys Ala Thr Leu
            115             120             125

Thr Pro Asp Ser Cys Tyr Pro Asp
    130             135
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 119 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Glu Gln Glu Tyr Ile Leu Ala Asn Asn Lys Cys Lys Cys Val Lys Ile
1               5               10              15

Ser Ser Arg Phe Val Pro Ser Thr Glu Arg Pro Gly Glu Glu Ile Leu
            20              25              30

Glu Arg Asn Ile Gln Ile Thr Ile Pro Thr Ser Ser Arg Met Xaa Ile
            35              40              45

Ser Asp Pro Tyr Ser Pro Leu Arg Thr Gln Pro Val Tyr Asn Leu Trp
        50              55              60

Asp Ile Cys Gln Lys Cys Asp Pro Val Gln Leu Glu Ile Gly Gly Ile
65              70              75              80

Pro Val Leu Ala Ser Gln Pro Xaa Xaa Ser Xaa Pro Asp Asp Glu Cys
            85              90              95

Tyr Thr Thr Glu Val Asn Phe Lys Lys Lys Val Pro Leu Thr Pro Asp
            100             105             110

Ser Cys Tyr Glu Tyr Ser Glu
            115
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 128 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Asn Lys Cys Met Cys Thr Arg Val Thr Ala Arg Ile Arg Gly Thr Arg
1               5               10              15

Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Tyr Ile Arg Ile Asn Val
            20              25              30

Pro Leu Lys Asn Arg Gly Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
            35              40              45

Asn Gln Pro Val Tyr His Leu Ser Pro Ser Cys Lys Lys Cys Asp Pro
        50              55              60
```

```
Tyr Glu Asp Gly Val Val Thr Ala Thr Glu Thr Asn Ile Cys Tyr Pro
65              70          75              80

Asp Gln Gly Val Pro Gln Ser Cys Arg Asp Tyr Cys Pro Glu Leu Asp
            85          90          95

Arg Asn Lys Cys Tyr Thr Val Leu Val Pro Pro Gly Tyr Thr Gly Glu
        100             105         110

Thr Lys Met Val Gln Asn Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
        115             120         125
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 421 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..414

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
GAT CAG GAA GAT GAA CGT ATT GTT CTG GTT GAC AAC AAG TGC AAG TGT      48
Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys
1               5               10              15

GCT CGT ATT ACT TCT AGA ATC ATC CGT AGC TCA GAG GAC CCA AAT GAA      96
Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu
            20              25              30

GAT ATA GTC GAA CGT AAC ATC CGT ATC ATC GTC CCA CTG AAT AAC CGG     144
Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg
        35              40              45

GAG AAT ATC TCA GAT CCT ACA AGT CCG TTG CGC ACA CGC TTC GTA TAC     192
Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr
        50              55              60

CAC CTG TCA GAT CTG TGT AAG AAG TGT GAT CCA ACA GAG GTA GAG CTG     240
His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu
65              70              75              80

GAC AAT CAG ATA GTC ACT GCG ACT CAA AGC AAC ATT TGC GAT GAG GAC     288
Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp
            85              90              95

AGC GCT ACA GAA ACC TGC AGC ACC TAC GAT AGG AAC AAA TGC TAC ACG     336
```

```
Ser Ala Thr Glu Thr Cys Ser Thr Tyr Asp Arg Asn Lys Cys Tyr Thr
        100                 105                 110
```

```
GCC GTG GTT CCG CTC GTG TAT GGT GGA GAG ACA AAA ATG GTG GAA ACT    384
Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr
        115                 120                 125
```

```
GCC CTT ACG CCC GAT GCA TGC TAT CCG GAC TGAATTC                    421
Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
        130                 135
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 215 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ix) FEATURE:
       (A) NAME/KEY: CDS
       (B) LOCATION: 1..213

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
GAT CAG AAG TGC AAG TGT GCT CGT ATT ACT TCT AGA ATC ATC CGT AGC    48
Asp Gln Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser
 1               5                  10                  15
```

```
TCA GAG GAC CCA AAT GAA GAT ATA GTC GAA CGT AAC ATC CGT ATC ATC    96
Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile
                20                  25                  30
```

```
GTC CCA CTG AAT AAC CGG GAG AAT ATC TCA GAT CCT ACA AGT CCG TTG    144
Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu
            35                  40                  45
```

```
CGC ACA CGC TTC GTA TAC CAC CTG TCA GAT CTG TGT AAG AAG GAT GAG    192
Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Asp Glu
        50                  55                  60
```

```
GAC AGC GCT ACA GAA ACC TGC TG                                     215
Asp Ser Ala Thr Glu Thr Cys
 65                  70
```

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 140 base pairs
       (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAGAATCAT CCGTAGCTCA GAGGACCCAA ATGAAGATAT AGTCGAACGT AACATCCGTA   60

TCATCGTCCC ACTGAATAAC CGGGAGAATA TCTCAGATCC TACAAGTCCG TTGCGCACAC   120

GCTTCGTATA CCACCTGTCA   140

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 31 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATCAGAAGT GCAAGTGTGC TCGTATTACT T   31

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 44 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..42

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAT CTG TGT AAG AAG GAT GAA GAT TCC GCT ACA GAA ACC TGC   42
Asp Leu Cys Lys Lys Asp Glu Asp Ser Ala Thr Glu Thr Cys
                75   80   85

TG   44

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 109 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
GCACCTACGA TAGGAACAAA TGCTACACGG CCGTGGTTCC GCTCGTGTAT GGTGGAGAGA       60

CAAAAATGGT GGAAACTGCC CTTACGCCCG ATGCATGCTA CCCTGACTG                  109
```

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 286 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..282

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
GAC AAC AAG TGC AAG TGT GCT CGT ATT ACT TCT AGA ATC ATC CGT AGC       48
Asp Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser
 15              20              25                  30

TCA GAG GAC CCA AAT GAA GAT ATA GTC GAA CGT AAC ATC CGT ATC ATC       96
Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile
                35              40              45

GTC CCA CTG AAT AAC CGG GAG AAT ATC TCA GAT CCT ACA AGT CCG TTG      144
Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu
                50              55              60

CGC ACA CGC TTC GTA TAC CAC CTG TCA GAT CTG TGT AAG AAG TGT GAT      192
Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp
            65              70              75

CCA ACA GAG GTA GAG CTG GAC AAT CAG ATA GTC ACT GCG ACT CAA AGC      240
Pro Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser
        80              85              90
```

```
AAC ATT TGC GAT GAG GAC AGC GCT ACA GAA ACC TGC TAC TGA          282
Asn Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr  *
 95                 100                 105

ATTC                                                             286
```

    (2) INFORMATION FOR SEQ ID NO:14:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 105 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ix) FEATURE:
            (A) NAME/KEY: CDS
            (B) LOCATION: 1..105

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
GAT CTG TGT AAG AAG TGT GAT CCA ACA GAG GTA GAG CTG GAC AAT CAG    48
Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp Asn Gln
 95                 100                 105                 110

ATA GTC ACT GCG ACT CAA AGC AAC ATT TGC GAT GAG GAC AGC GCT ACA    96
Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser Ala Thr
                115                 120                 125

CTT TGG ACG                                                      105
Leu Trp Thr
```


    (2) INFORMATION FOR SEQ ID NO:15:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 61 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
GATCAGGAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGTGTGC TCGTATTACT    60

T                                                                  61
```

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 198 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
GCGATGACGA CGATAAGGCC CAAACGGAGA CCTGTACTGT TGCGCCTCGT GAACGGCAAA        60

ACTGCGGATT CCCGGAAGTA ACACCCTCTC AGTGCGCTAA TAAAGGCTGC TGTTTTGATG       120

ACACGGTACG GGGCGTTCCG TGGTGCTTCT ACCCCAATAC AATTGACGTT CCGCCTGAAG       180

AAGAGTGCGA GCCGTAAG                                                     198
```

(2) INFORMATION FOR SEQ ID NO:17:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 138 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys
  1           5               10              15

Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu
            20              25              30

Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg
            35              40              45

Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr
  50              55              60

His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu
  65              70              75              80

Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp
                85              90              95

Ser Ala Thr Glu Thr Cys Ser Thr Tyr Asp Arg Asn Lys Cys Tyr Thr
            100             105             110
```

Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr
     115   120   125

Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
     130   135

(2) INFORMATION FOR SEQ ID NO:18:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 71 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asp Gln Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser
  1   5   10   15

Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile
         20   25   30

Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu
     35   40   45

Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Asp Glu
     50   55   60

Asp Ser Ala Thr Glu Thr Cys
  65   70

(2) INFORMATION FOR SEQ ID NO:19:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 49 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp Ile Val Glu
  1   5   10   15

Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu Asn Ile Ser
         20   25   30

Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr His Leu Ser Asp
         35   40   45

Leu

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Asp Gln Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 14 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Asp Leu Cys Lys Lys Asp Glu Asp Ser Ala Thr Glu Thr Cys
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Ser Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val
1               5                   10                  15

Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala
                20                  25                  30
```

```
           Cys Tyr Pro Asp
                    35
```

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 93 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
Asp Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser
 1               5                  10                  15

Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile
            20                  25                  30

Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu
        35                  40                  45

Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp
    50                  55                  60

Pro Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser
65                  70                  75                  80

Asn Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr
            85                  90
```

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp Asn Gln
 1               5                  10                  15

Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser Ala Thr
            20                  25                  30

Leu Trp Thr
        35
```

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys
1   5   10   15

Ala Arg Ile Thr Ser Arg
        20

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 66 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Ser Asp Asp Asp Asp Lys Ala Gln Thr Glu Thr Cys Thr Val Ala
1   5   10   15

Pro Arg Glu Arg Gln Asn Cys Gly Phe Pro Gly Val Thr Pro Ser Gln
        20   25   30

Cys Ala Asn Lys Gly Cys Cys Phe Asp Asp Thr Val Arg Gly Val Pro
        35   40   45

Trp Cys Phe Tyr Pro Asn Thr Ile Asp Val Pro Pro Glu Glu Glu Cys
   50   55   60

Glu Phe
65

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 421 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
CTAGTCCTTC TACTTGCATA ACAAGACCAA CTGTTGTTCA CGTTCACACG AGCATAATGA        60

AGATCTTAGT AGGCATCGAG TCTCCTGGGT TTACTTCTAT ATCAGCTTGC ATTGTAGGCA       120

TAGTAGCAGG GTGACTTATT GGCCCTCTTA TAGAGTCTAG GATGTTCAGG CAACGCGTGT       180

GCGAAGCATA TGGTGGACAG TCTAGACACA TTCTTCACAC TAGGTTGTCT CCATCTCGAC       240

CTGTTAGTCT ATCAGTGACG CTGAGTTTCG TTGTAAACGC TACTCCTGTC GCGATGTCTT       300

TGGACGTCGT GGATGCTATC CTTGTTTACG ATGTGCCGGC ACCAAGGCGA GCACATACCA       360

CCTCTCTGTT TTTACCACCT TTGACGGGAA TGCGGGCTAC GTACGATAGG CCTGACTTAA       420

G                                                                      421
```

(2) INFORMATION FOR SEQ ID NO:28:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 219 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
CTAGTCTTCA CGTTCACACG AGCATAATGA AGATCTTAGT AGGCATCGAG TCTCCTGGGT        60

TTACTTCTAT ATCAGCTTGC ATTGTAGGCA TAGTAGCAGG GTGACTTATT GGCCCTCTTA       120

TAGAGTCTAG GATGTTCAGG CAACGCGTGT GCGAAGCATA TGGTGGACAG TCTAGACACA       180

TTCTTCCTAC TCCTGTCGCG ATGTCTTTGG ACGACTTAA                              219
```

(2) INFORMATION FOR SEQ ID NO:29:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 140 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTAGTAGGCA TCGAGTCTCC TGGGTTTACT TCTATATCAG CTTGCATTGT AGGCATAGTA   60

GCAGGGTGAC TTATTGGCCC TCTTATAGAG TCTAGGATGT TCAGGCAACG CGTGTGCGAA   120

GCATATGGTG GACAGTCTAG   140

(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 31 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCTTCACGTT CACACGAGCA TAATGAAGAT C   31

(2) INFORMATION FOR SEQ ID NO:31:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 44 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ACACATTCTT CCTACTTCTC AGGCGATGTC TTTGGACGAC TTAA   44

(2) INFORMATION FOR SEQ ID NO:32:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 117 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACGTCGTGGA TGCTATCCTT GTTTACGATG TGCCGGCACC AAGGCGAGCA CATACCACCT   60

CTCTGTTTTT ACCACCTTTG ACGGGAATGC GGGCTACGTA CGATGGGACT GACTTAA   117

(2) INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 282 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGTTGTTCA CGTTCACACG AGCATAATGA AGATCTTAGT AGGCATCGAG TCTCCTGGGT   60

TTACTTCTAT ATCAGCTTGC ATTGTAGGCA TAGTAGCAGG GTGACTTATT GGCCCTCTTA   120

TAGAGTCTAG GATGTTCAGG CAACGCGTGT GCGAAGCATA TGGTGGACAG TCTAGACACA   180

TTCTTCACAC TAGGTTGTCT CCATCTCGAC CTGTTAGTCT ATCAGTGACG CTGAGTTTCG   240

TTGTAAACGC TACTCCTGTC GCGATGTCTT TGGACGATGA CT   282

(2) INFORMATION FOR SEQ ID NO:34:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 105 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCTGTGTA AGAAGTGTGA TCCAACAGAG GTAGAGCTGG ACAATCAGAT AGTCACTGCG   60

ACTCAAAGCA ACATTTGCGA TGAGGACAGC GCTACACTTT GGACG   105

(2) INFORMATION FOR SEQ ID NO:35:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 65 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CTAGTCCTTC TACTTGCATA ACAAGACCAA CTGTTGTTCA CGTTCACACG AGCATAATGA   60

AGATC   65

(2) INFORMATION FOR SEQ ID NO:36:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 206 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACTTCGCTAC TGCTGCTATT CCGGGTTTGC CTCTGGACAT GACAACGCGG AGCACTTGCC   60

GTTTTGACGC CTAAGGGCCT TCATTGTGGG AGAGTCACGC GATTATTTCC GACGACAAAA   120

CTACTGTGCC ATGCCCCGCA AGGCACCACG AAGATGGGGT TATGTTAACT GCAAGGCGGA   180

CTTCTTCTCA CGCTCGGCAT TCTTAA   206

(2) INFORMATION FOR SEQ ID NO:37:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys
1   5   10

(2) INFORMATION FOR SEQ ID NO:38:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 7 amino acids
        (B) TYPE: amino acid

```
              (C)  STRANDEDNESS:
              (D)  TOPOLOGY: linear
```

```
    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:38:

    Glu Asn Leu Tyr Phe Gln Ser
    1               5
```

(2) INFORMATION FOR SEQ ID NO:39:

```
    (i)  SEQUENCE CHARACTERISTICS:
              (A)  LENGTH: 11 amino acids
              (B)  TYPE: amino acid
              (C)  STRANDEDNESS:
              (D)  TOPOLOGY: linear
```

```
    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:39:

    Lys Ala His Lys Val Asp Met Val Gln Tyr Thr
    1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:40:

```
    (i)  SEQUENCE CHARACTERISTICS:
              (A)  LENGTH: 4 amino acids
              (B)  TYPE: amino acid
              (C)  STRANDEDNESS:
              (D)  TOPOLOGY: linear
```

```
    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:40:

    Val Gln Tyr Thr
    1
```

(2) INFORMATION FOR SEQ ID NO:41:

```
    (i)  SEQUENCE CHARACTERISTICS:
              (A)  LENGTH: 6 amino acids
              (B)  TYPE: amino acid
              (C)  STRANDEDNESS:
              (D)  TOPOLOGY: linear
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu Lys Ala Val Ala Asp
1   5

(2) INFORMATION FOR SEQ ID NO:42:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 131 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..78

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
ATG AAA TTC TTA GTC AAC GTT GCC CTT TTT ATG GTC GTA TAC ATT TCT        48
Met Lys Phe Leu Val Asn Val Ala Leu Phe Met Val Val Tyr Ile Ser
              40                  45                  50

TAC ATC TAT GCG GAT CCG AGC TCG AGT GCT CTAGATCTGC AGCTGGTACC         98
Tyr Ile Tyr Ala Asp Pro Ser Ser Ser Ala
              55                  60

ATGGAATTCG AAGCTTGGAG TCGACTCTGC TGA                                   131
```

(2) INFORMATION FOR SEQ ID NO:43:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
Met Lys Phe Leu Val Asn Val Ala Leu Phe Met Val Val Tyr Ile Ser
 1               5                  10                  15

Tyr Ile Tyr Ala Asp Pro Ser Ser Ser Ala
              20                  25
```

(2) INFORMATION FOR SEQ ID NO:44:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

    Lys Asp Glu Leu
    1

(2) INFORMATION FOR SEQ ID NO:45:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

    Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu Lys Ala Val Ala Asp
     1   5   10   15

(2) INFORMATION FOR SEQ ID NO:46:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 61 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GATCAGGAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGTGTGC TCGTATTACT   60

T   61

(2) INFORMATION FOR SEQ ID NO:47:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 61 base pairs

            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTAGAAGTAA TACGAGCACA CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC   60

T   61

(2) INFORMATION FOR SEQ ID NO:48:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 31 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCAGAAGT GCAAGTGTGC TCGTATTACT T   31

(2) INFORMATION FOR SEQ ID NO:49:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 31 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTAGAAGTAA TACGAGCACA CTTGCACTTC T   31

(2) INFORMATION FOR SEQ ID NO:50:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 61 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGTCCGC TCGTATTACT   60

T   61

(2) INFORMATION FOR SEQ ID NO:51:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 61 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTAGAAGTAA TACGAGCGGA CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC   60

T   61

(2) INFORMATION FOR SEQ ID NO:52:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 61 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCAGGAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGGTTGC TCGTATTACT   60

T   61

(2) INFORMATION FOR SEQ ID NO:53:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 61 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTAGAAGTAA TACGAGCAAC CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC   60

T   61

(2) INFORMATION FOR SEQ ID NO:54:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 47 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTAGAATCAT CCGTAGCTCA GAGGACCCAA ATGAAGATAT AGTCGAA   47

(2) INFORMATION FOR SEQ ID NO:55:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 58 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATACGGATG TTACGTTCGA CTATATCTTC ATTTGGGTCC TCTGAGCTAC GGATGATT   58

(2) INFORMATION FOR SEQ ID NO:56:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 49 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGTAACATCC GTATCATCGT CCCACTGAAT AACCGGGAGA ATATCTCAG   49

(2) INFORMATION FOR SEQ ID NO:57:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 49 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGTAACATCC GTATCATCGT CCCACTGAAT AACCGGGAGC ACATCTCAG   49

(2) INFORMATION FOR SEQ ID NO:58:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 49 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACGGACTTGT AGGATCTGAG ATATTCTCCC GGTTATTCAG TGGGACGAT   49

(2) INFORMATION FOR SEQ ID NO:59:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 49 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACGGACTTGT AGGATCTGAG ATGTGCTCCC GGTTATTCAG TGGGACGAT   49

(2) INFORMATION FOR SEQ ID NO:60:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 44 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATCCTACAAG TCCGTTGCGC ACACGCTTCG TATACCACCT GTCA   44

(2) INFORMATION FOR SEQ ID NO:61:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 33 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GATCTGACAG GTGGTATACG AAGCGTGTGC GCA   33

(2) INFORMATION FOR SEQ ID NO:62:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 60 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GATCTGTGTA AGAAGTGTGA TCCAACAGAG GTAGAGCTGG ACAATCAGAT AGTCACTGCA   60

(2) INFORMATION FOR SEQ ID NO:63:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 44 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GATCTGTGTA AGAAGGATGA GGACAGCGCT ACAGAAACCT GCTG   44

(2) INFORMATION FOR SEQ ID NO:64:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 44 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

AATTCAGCAG GTTTCTGTAG CGCTGTCCTC ATCCTTCTTA CACA   44

(2) INFORMATION FOR SEQ ID NO:65:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 62 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GATCTGTGTA AGAAGGATGA GGACAGCGCT ACAGAAACCT GCTACGAGAA GGATGAGCTG   60

TG   62

(2) INFORMATION FOR SEQ ID NO:66:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 62 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AATTCACAGC TCATCCTTCG CGTCGCAGGT TTCTGTAGCG CTGTCCTCAT CCTTCTTACA   60

CA   62

(2) INFORMATION FOR SEQ ID NO:67:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCTGTGTA AGAAGTCTGA TATCGATGAA GATTCCGCTA CAGAAACCTG CAGCACATG   59

(2) INFORMATION FOR SEQ ID NO:68:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AATTCATGTG CTGCAGGTTT CTGTAGCGGA ATCTTCATCG ATATCAGACT TCTTACACA   59

(2) INFORMATION FOR SEQ ID NO:69:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 64 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GATCTGTCTA AGAAGTCTGA TATCGATGAA GATTACAGAT TCTTCAGACT ATAGCTACTT   60

CTAA   64

(2) INFORMATION FOR SEQ ID NO:70:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AATCTTCATC GATATCAGAC TTCTTAGACA   30

(2) INFORMATION FOR SEQ ID NO:71:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 64 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GATCTGGTTA AGAAGTCTGA TATCGATGAA GATTACCAAT TCTTCAGACT ATAGCTACTT   60

CTAA   64

(2) INFORMATION FOR SEQ ID NO:72:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AATCTTCATC GATATCAGAC TTCTTAACCA   30

(2) INFORMATION FOR SEQ ID NO:73:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 41 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTGTCCAGC TCTACCTCTG TTGGATCACA CTTCTTACAC A   41

(2) INFORMATION FOR SEQ ID NO:74:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACTCAAAGCA ACATTTGCGA TGAGGACAGC GCTACAGAAA CCTGCA   46

(2) INFORMATION FOR SEQ ID NO:75:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 57 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GGTTTCTGTA GCGCTCTGCT CATCGCAAAT GTTGCTTTGA GTCGCAGTGA CTATCTG   57

(2) INFORMATION FOR SEQ ID NO:76:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 59 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GCACCTACGA TAGGAACAAA TGCTACACGG CCGTGGTTCC GCTCGTGTAT GGTGGAGAG   59

(2) INFORMATION FOR SEQ ID NO:77:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 48 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GAGCGGAACC ACGGCCGTGT AGCATTTGTT CCTATCGTAG GTGCTGCA   48

(2) INFORMATION FOR SEQ ID NO:78:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 50 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACAAAAATGG TGGAAACTGC CCTTACGCCC GATGCATGCT ATCCGGACTG   50

(2) INFORMATION FOR SEQ ID NO:79:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 69 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AATTCAGTCC GGATAGCATG CATCGGGCGT AAGGGCAGTT TCCACCATTT TTGTCTCTCC   60

ACCATACAC   69

(2) INFORMATION FOR SEQ ID NO:80:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 62 base pairs
        (B) TYPE: nucleic acid

            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAAAAATGG TGGAAACTGC CCTTACGCCC GATGCATGCT ATCCGGACAA GGATGAATTG   60

TG   62

(2) INFORMATION FOR SEQ ID NO:81:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 81 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AATTCACAAT TCATCCTTGT CCGGATAGCA TGCATCGGGC GTAAGGGCAG TTTCCACCAT   60

TTTTGTCTCT CCACCATACA C   81

(2) INFORMATION FOR SEQ ID NO:82:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 88 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GATCAGGTCG CTGCCATCCA AGACCCGAGG CTGTTCGCCG AAGAGAAGGC CGTCGCTGAC   60

TCCAAGTGCA AGTGTGCTCG TATTACTT   88

(2) INFORMATION FOR SEQ ID NO:83:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 88 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CTAGAAGTAA TACGAGCACA CTTGCACTTG GAGTCAGCGA CGGCCTTCTC TTCGGCGAAC   60

AGCCTCGGGT CTTGGATGGC AGCGACCT   88

(2) INFORMATION FOR SEQ ID NO:84:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Cys Ala Ala Pro Lys Lys Lys Arg Lys Val
1   5   10

(2) INFORMATION FOR SEQ ID NO:85:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Cys Ala Ala Lys Arg Pro Pro Ala Ala Ile Lys Lys Ala Ala Ala Gly
1   5   10   15

Gln Ala Lys Lys Lys Lys
              20

(2) INFORMATION FOR SEQ ID NO:86:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

His Asp Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:87:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 77 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCGATGACGA CGATAAGGCC CAAACGGAGA CCTGTACTGT TGCGCCTCGT GAACGGCAAA   60

ACTGCGGATT CCCGGAA   77

(2) INFORMATION FOR SEQ ID NO:88:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 66 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTTTTGCCGT TCACGAGGCG CAACAGTACA GGTCTCCGTT TGGGCCTTAT CGTCGTCATC   60

GCTTCA   66

(2) INFORMATION FOR SEQ ID NO:89:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 72 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTAACACCCT CTCAGTGCGC TAATAAAGGC TGCTGTTTTG ATGACACGGT ACGGGGCGTT   60

CCGTGGTGCT TC   72

(2) INFORMATION FOR SEQ ID NO:90:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 72 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCCCCGTACC GTGTCATCAA AACAGCAGCC TTTATTAGCG CACTGAGAGG GTGTTACTTC   60

CGGGAATCCG CA   72

(2) INFORMATION FOR SEQ ID NO:91:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 49 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TACCCCAATA CAATTGACGT TCCGCCTGAA GAAGAGTGCG AGCCGTAAG   49

(2) INFORMATION FOR SEQ ID NO:92:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 68 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

AATTCTTACG GCTCGCACTC TTCTTCAGGC GGCAAGTCAA TTGTATTGGG GTAGAAGCAC   60

CACGGAAC   68

(2) INFORMATION FOR SEQ ID NO:93:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Val Ala Val Gln Ser Ala Gly Thr Pro Ala Ser Gly Ser
1   5   10